RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number:	08/252, 384c
Source:	IFW16
Date Processed by STIC:	11/10/2005
	/

ENTERED



IFW

RAW SEQUENCE LISTING DATE: 11/10/2005
PATENT APPLICATION: US/08/252,384C TIME: 12:22:35

Input Set : A:\seq listing.txt

```
3 <110> APPLICANT: Reactive Surfaces, Ltd.
        McDaniel, Steven
        Raushel, Frank M
        Wild, James R
8 <120> TITLE OF INVENTION: Recombinant Organophosphorous Acid Anhydrase and Methods of Use
10 <130> FILE REFERENCE: TAMK145
12 <140> CURRENT APPLICATION NUMBER: US 08/252,384C
13 <141> CURRENT FILING DATE: 1994-06-01
15 <150> PRIOR APPLICATION NUMBER: US 07/928,540
16 <151> PRIOR FILING DATE: 1992-08-13
18 <150> PRIOR APPLICATION NUMBER: US 07/344,258
19 <151> PRIOR FILING DATE: 1989-04-27
21 <160> NUMBER OF SEQ ID NOS: 2
23 <170> SOFTWARE: PatentIn version 3.3
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 1337
27 <212> TYPE: DNA
28 <213> ORGANISM: Pseudomonas diminuta
31 <220> FEATURE:
32 <221> NAME/KEY: CDS
33 <222> LOCATION: (63)..(1160)
35 <400> SEQUENCE: 1
                                                                          60
36 ctgcagcctg actcggcacc agtcgctgca agcagagtcg taagcaatcg caagggggca
                                                                         107
38 gc atg caa acg aga agg gtt gtg ctc aag tct gcg gcc gcc gca gga
     Met Gln Thr Arg Arg Val Val Leu Lys Ser Ala Ala Ala Gly
40
42 act ctg ctc ggc ggc ctg gct ggg tgc gcg agc gtg gct gga tcg atc
                                                                         155
43 Thr Leu Leu Gly Gly Leu Ala Gly Cys Ala Ser Val Ala Gly Ser Ile
                                                                         203
46 qgc aca ggc gat cgg atc aat acc gtg cgc ggt cct atc aca atc tct
47 Gly Thr Gly Asp Arg Ile Asn Thr Val Arg Gly Pro Ile Thr Ile Ser
               35
48
50 gaa gcg ggt ttc aca ctg act cac gag cac atc tgc ggc agc tcg gca
                                                                         251
51 Glu Ala Gly Phe Thr Leu Thr His Glu His Ile Cys Gly Ser Ser Ala
                                                                         299
54 gga ttc ttg cgt gct tgg cca gag ttc ttc ggt agc cgc aaa gct cta
55 Gly Phe Leu Arg Ala Trp Pro Glu Phe Phe Gly Ser Arg Lys Ala Leu
                                                                         347
58 gcg gaa aag gct gtg aga gga ttg cgc cgc gcc aga gcg gct ggc gtg
59 Ala Glu Lys Ala Val Arg Gly Leu Arg Arg Ala Arg Ala Ala Gly Val
60 80
                       85
                                                                         395
62 cga acg att gtc gat gtg tcg act ttc gat atc ggt cgc gac gtc agt
63 Arq Thr Ile Val Asp Val Ser Thr Phe Asp Ile Gly Arg Asp Val Ser
```

RAW SEQUENCE LISTING DATE: 11/10/2005
PATENT APPLICATION: US/08/252,384C TIME: 12:22:35

Input Set : A:\seq listing.txt

64 100 105 110	
66 tta ttg gcc gag gtt tcg cgg gct gcc gac gtt cat atc gtg gcg	443
67 Leu Leu Ala Glu Val Ser Arg Ala Ala Asp Val His Ile Val Ala Ala	443
68 115 120 125	
70 acc ggc ttg tgg ttc gac ccg cca ctt tcg atg cga ttg agg agt gta	491
71 Thr Gly Leu Trp Phe Asp Pro Pro Leu Ser Met Arg Leu Arg Ser Val	471
72 130 135 140	
74 gag gaa ctc aca cag ttc ttc ctg cgt gag att caa tat ggc atc gaa	539
75 Glu Glu Leu Thr Gln Phe Phe Leu Arg Glu Ile Gln Tyr Gly Ile Glu	333
76 145 150 155	
78 gac acc gga att agg gcg ggc att atc aag gtc gcg acc aca ggc aag	587
79 Asp Thr Gly Ile Arg Ala Gly Ile Ile Lys Val Ala Thr Thr Gly Lys	
80 160 165 170 175	
82 gcg acc ccc ttt cag gag tta gtg tta aag gcg gcc gcc cgg gcc agc	635
83 Ala Thr Pro Phe Gln Glu Leu Val Leu Lys Ala Ala Arg Ala Ser	
84 180 185 190	
86 ttg gcc acc ggt gtt ccg gta acc act cac acg gca gca agt cag cgc	683
87 Leu Ala Thr Gly Val Pro Val Thr Thr His Thr Ala Ala Ser Gln Arg	
88 195 200 205	
90 gat ggt gag cag cag gcc gcc att ttt gag tcc gaa ggc ttg agc ccc	731
91 Asp Gly Glu Gln Gln Ala Ala Ile Phe Glu Ser Glu Gly Leu Ser Pro	
92 210 215 220	
94 tca cgg gtt tgt att ggt cac agc gat gat act gac gat ttg agc tat	779
95 Ser Arg Val Cys Ile Gly His Ser Asp Asp Thr Asp Asp Leu Ser Tyr	
96 225 230 235	
98 ctc acc gcc ctc gct gcg cgc gga tac ctc atc ggt cta gac cac atc	827
98 ctc acc gcc ctc gct gcg cgc gga tac ctc atc ggt cta gac cac atc 99 Leu Thr Ala Leu Ala Ala Arg Gly Tyr Leu Ile Gly Leu Asp His Ile	827
	827
99 Leu Thr Ala Leu Ala Ala Arg Gly Tyr Leu Ile Gly Leu Asp His Ile	827 875
99 Leu Thr Ala Leu Ala Ala Arg Gly Tyr Leu Ile Gly Leu Asp His Ile 100 240 245 250 255	
99 Leu Thr Ala Leu Ala Ala Arg Gly Tyr Leu Ile Gly Leu Asp His Ile 100 240 245 250 255 102 ccg cac agt gcg att ggt cta gaa gat aat gcg agt gca tca gcc ctc	
99 Leu Thr Ala Leu Ala Ala Arg Gly Tyr Leu Ile Gly Leu Asp His Ile 100 240 245 250 255 102 ccg cac agt gcg att ggt cta gaa gat aat gcg agt gca tca gcc ctc 103 Pro His Ser Ala Ile Gly Leu Glu Asp Asn Ala Ser Ala Ser Ala Leu 104 260 265 270 106 ctg ggc atc cgt tcg tgg caa aca cgg gct ctc ttg atc aag gcg ctc	
99 Leu Thr Ala Leu Ala Ala Arg Gly Tyr Leu Ile Gly Leu Asp His Ile 100 240 245 250 255 102 ccg cac agt gcg att ggt cta gaa gat aat gcg agt gca tca gcc ctc 103 Pro His Ser Ala Ile Gly Leu Glu Asp Asn Ala Ser Ala Ser Ala Leu 104 260 265 270 106 ctg ggc atc cgt tcg tgg caa aca cgg gct ctc ttg atc aag gcg ctc 107 Leu Gly Ile Arg Ser Trp Gln Thr Arg Ala Leu Leu Ile Lys Ala Leu	875
99 Leu Thr Ala Leu Ala Ala Arg Gly Tyr Leu Ile Gly Leu Asp His Ile 100 240 245 250 255 102 ccg cac agt gcg att ggt cta gaa gat aat gcg agt gca tca gcc ctc 103 Pro His Ser Ala Ile Gly Leu Glu Asp Asn Ala Ser Ala Ser Ala Leu 104 260 265 270 106 ctg ggc atc cgt tcg tgg caa aca cgg gct ctc ttg atc aag gcg ctc 107 Leu Gly Ile Arg Ser Trp Gln Thr Arg Ala Leu Leu Ile Lys Ala Leu 108 275 280 285	875 923
99 Leu Thr Ala Leu Ala Ala Arg Gly Tyr Leu Ile Gly Leu Asp His Ile 100 240 245 250 255 102 ccg cac agt gcg att ggt cta gaa gat aat gcg agt gca tca gcc ctc 103 Pro His Ser Ala Ile Gly Leu Glu Asp Asn Ala Ser Ala Ser Ala Leu 104 260 265 270 106 ctg ggc atc cgt tcg tgg caa aca cgg gct ctc ttg atc aag gcg ctc 107 Leu Gly Ile Arg Ser Trp Gln Thr Arg Ala Leu Leu Ile Lys Ala Leu 108 275 280 285 110 atc gac caa ggc tac atg aaa caa atc ctc gtt tcg aat gac tgg ctg	875
99 Leu Thr Ala Leu Ala Ala Arg Gly Tyr Leu Ile Gly Leu Asp His Ile 100 240 245 250 255 102 ccg cac agt gcg att ggt cta gaa gat aat gcg agt gca tca gcc ctc 103 Pro His Ser Ala Ile Gly Leu Glu Asp Asn Ala Ser Ala Ser Ala Leu 104 260 265 270 106 ctg ggc atc cgt tcg tgg caa aca cgg gct ctc ttg atc aag gcg ctc 107 Leu Gly Ile Arg Ser Trp Gln Thr Arg Ala Leu Leu Ile Lys Ala Leu 108 275 280 285 110 atc gac caa ggc tac atg aaa caa atc ctc gtt tcg aat gac tgg ctg 111 Ile Asp Gln Gly Tyr Met Lys Gln Ile Leu Val Ser Asn Asp Trp Leu	875 923
99 Leu Thr Ala Leu Ala Ala Arg Gly Tyr Leu Ile Gly Leu Asp His Ile 100 240	875 923 971
99 Leu Thr Ala Leu Ala Ala Arg Gly Tyr Leu Ile Gly Leu Asp His Ile 100 240	875 923
99 Leu Thr Ala Leu Ala Ala Arg Gly Tyr Leu Ile Gly Leu Asp His Ile 100 240	875 923 971
99 Leu Thr Ala Leu Ala Ala Arg Gly Tyr Leu Ile Gly Leu Asp His Ile 100 240	875 923 971 1019
99 Leu Thr Ala Leu Ala Ala Arg Gly Tyr Leu Ile Gly Leu Asp His Ile 100 240	875 923 971
99 Leu Thr Ala Leu Ala Ala Arg Gly Tyr Leu Ile Gly Leu Asp His Ile 100 240	875 923 971 1019
99 Leu Thr Ala Leu Ala Ala Arg Gly Tyr Leu Ile Gly Leu Asp His Ile 100 240	875 923 971 1019
99 Leu Thr Ala Leu Ala Ala Arg Gly Tyr Leu Ile Gly Leu Asp His Ile 100 240 245 250 255 102 ccg cac agt gcg att ggt cta gaa gat aat gcg agt gca tca gcc ctc 103 Pro His Ser Ala Ile Gly Leu Glu Asp Asn Ala Ser Ala Ser Ala Leu 104 260 265 270 106 ctg ggc atc cgt tcg tgg caa aca cgg gct ctc ttg atc aag gcg ctc 107 Leu Gly Ile Arg Ser Trp Gln Thr Arg Ala Leu Leu Ile Lys Ala Leu 108 275 280 285 110 atc gac caa ggc tac atg aaa caa atc ctc gtt tcg aat gac tgg ctg 111 Ile Asp Gln Gly Tyr Met Lys Gln Ile Leu Val Ser Asn Asp Trp Leu 112 290 295 300 114 ttc ggg ttt tcg agc tat gtc acc aac atc atg gac gtg atg gcc 115 Phe Gly Phe Ser Ser Tyr Val Thr Asn Ile Met Asp Val Met Asp Arg 116 305 310 315 118 gtg aac ccc gac ggg atg gcc ttc att cca ctg aga gtg atc cca ttc 119 Val Asn Pro Asp Gly Met Ala Phe Ile Pro Leu Arg Val Ile Pro Phe 120 320 325 330 335 122 cta cga gag aag ggc gtc cca caa acc ccg gca ggc atc acc gtg	875 923 971 1019
99 Leu Thr Ala Leu Ala Ala Arg Gly Tyr Leu Ile Gly Leu Asp His Ile 100 240 245 250 255 102 ccg cac agt gcg att ggt cta gaa gat aat gcg agt gca tca gcc ctc 103 Pro His Ser Ala Ile Gly Leu Glu Asp Asn Ala Ser Ala Ser Ala Leu 104 260 265 270 106 ctg ggc atc cgt tcg tgg caa aca cgg gct ctc ttg atc aag gcg ctc 107 Leu Gly Ile Arg Ser Trp Gln Thr Arg Ala Leu Leu Ile Lys Ala Leu 108 275 280 285 110 atc gac caa ggc tac atg aaa caa atc ctc gtt tcg aat gac tgg ctg 111 Ile Asp Gln Gly Tyr Met Lys Gln Ile Leu Val Ser Asn Asp Trp Leu 112 290 295 300 114 ttc ggg ttt tcg agc tat gtc acc aac atc atc atg gac gtg atg gat cgc 115 Phe Gly Phe Ser Ser Tyr Val Thr Asn Ile Met Asp Val Met Asp Arg 116 305 310 315 118 gtg aac ccc gac ggg atg gcc ttc att cca ctg aga gtg atc cca ttc 119 Val Asn Pro Asp Gly Met Ala Phe Ile Pro Leu Arg Val Ile Pro Phe 120 320 325 335 122 cta cga gag aag ggc gtc cca cag gaa acg ctg gca ggc atc act gtg 123 Leu Arg Glu Lys Gly Val Pro Gln Glu Thr Leu Ala Gly Ile Thr Val	875 923 971 1019
99 Leu Thr Ala Leu Ala Ala Arg Gly Tyr Leu Ile Gly Leu Asp His Ile 100 240	875 923 971 1019 1067
99 Leu Thr Ala Leu Ala Ala Arg Gly Tyr Leu Ile Gly Leu Asp His Ile 100 240	875 923 971 1019
99 Leu Thr Ala Leu Ala Ala Arg Gly Tyr Leu Ile Gly Leu Asp His Ile 100 240	875 923 971 1019 1067

RAW SEQUENCE LISTING DATE: 11/10/2005
PATENT APPLICATION: US/08/252,384C TIME: 12:22:35

Input Set : A:\seq listing.txt

130 cgccatctgg atccttccag ccagcggcca ctattcccg tcaagtacc gaacgtagaa 1220 ' 132 gtcagccatc gatgataga catcttcaat ttgatcaggg ctgccacctc caaagccgtg 1280 134 gccaccctg tcgatagtct tgaggacgta gggcacacg tgcttttcga actgcag 1280 137 <210> SEQ ID NO: 2 138 <211> LENGTH: 365 139 <212> TYPE: PRT 140 <213> ORGANISM: Pseudomonas diminuta 142 <400> SEQUENCE: 2 144 Met Gln Thr Arg Arg Val Val Leu Lys Ser Ala Ala Ala Ala Gly Thr 145 15																			
134 gccaccctg tcgatagtet tgaggacgta gggcacaccg tgcttttcga actgcag 137 <210> SEQ ID NO: 2 138 <211> LENGTH: 365 139 <212> TYPE: PRT 140 <213> ORGANISM: Pseudomonas diminuta 142 <400> SEQUENCE: 2 144 Met Gln Thr Arg Arg Val Val Leu Lys Ser Ala Ala Ala Ala Gly Thr 145		_					_					_		_	_	-		1220	•
137		_		_	-	-				_	-		_			_		1280	
138	13	l gccacccctg tcgatagtct tgaggacgta gggcacaccg tgcttttcga actgcag										1337							
139																			
140	13	<21	<211> LENGTH: 365																
142	13	<21	<212> TYPE: PRT																
144 Met Gln Thr Arg Arg Arg Val Leu Lys Ser Ala Ala Ala Ala Ala Gly Thr 145 1	. 14	<21																	
148 Leu Leu Gly Gly Leu Ala Gly Cys Ala Ser Val Ala Gly Ser Ile Gly Gly Ser Ile Gly Gly	14																		
148 Leu Leu Gly Gly Leu Ala Gly Cys Ala Ser Val Ala Gly Ser Ile Gly 149 20 25 30 152 Thr Gly Asp Arg Ile Asn Thr Val Arg Gly Pro Ile Thr Ile Ser Glu 153 35 40 40 45 156 Ala Gly Phe Thr Leu Thr His Glu His Ile Cys Gly Ser Ser Ala Gly 157 50 50 55 60 160 Phe Leu Arg Ala Trp Pro Glu Phe Phe Gly Ser Arg Lys Ala Leu Ala 161 65 70 75 85 90 95 164 Glu Lys Ala Val Arg Gly Leu Arg Arg Ala Arg Ala Arg Ala Gly Val Arg 165 85 95 95 168 Thr Ile Val Asp Val Ser Thr Phe Asp Ile Gly Arg Asp Val Ser Leu 169 100 105 110 172 Leu Ala Glu Val Ser Arg Ala Ala Asp Val His Ile Val Ala Ala Thr 130 115 120 125 176 Gly Leu Trp Phe Asp Pro Pro Leu Ser Met Arg Leu Arg Ser Val Glu 177 130 135 150 150 184 Thr Gly Ile Arg Ala Gly Ile Ile Lys Val Ala Thr Thr Gly Lys Ala 165 165 165 165 165 165 165 165 165 165	14	Met	Gln	Thr	Arg	Arg	Val	Val	Leu	Lys	Ser	Ala	Ala	Ala	Ala	Gly	Thr		
149	14	5 1				5					10					15			
The Secondaria The Secondaria Seco	14	3 Leu	Leu	Gly	Gly	Leu	Ala	Gly	Cys	Ala	Ser	Val	Ala	Gly	Ser	Ile	Gly		
153	14	€			20					25					30				
The second color of the	15	? Thr	Gly	Asp	Arg	Ile	Asn	Thr	Val	Arg	Gly	Pro	Ile	Thr	Ile	Ser	Glu		
157	15	3		35					40					45					
160	15	6 Ala	Gly	Phe	Thr	Leu	Thr	His	Glu	His	Ile	Cys	Gly	Ser	Ser	Ala	Gly		
161 65	15	7	50					55					60						
The color of the	16) Phe	Leu	Arg	Ala	Trp	Pro	Glu	Phe	Phe	Gly	Ser	Arg	Lys	Ala	Leu	Ala		
165	16	L 65					70					75					80		
168	16	: Glu	Lys	Ala	Val	Arg	Gly	Leu	Arg	Arg	Ala	Arg	Ala	Ala	Gly	Val	Arg		
169	16	5				85					90					95			
172 Leu Ala Glu Val Ser Arg Ala Ala Ala Asp Val His Ile Val Ala Ala	16	3 Thr	Ile	Val	Asp	Val	Ser	Thr	Phe	Asp	Ile	Gly	Arg	Asp	Val	Ser	Leu		
173 115 120 125 125 126 125 140	16	€			100					105					110				
176 Gly Leu Trp Phe Asp Pro Pro Leu Ser Met Arg Leu Arg Ser Val Glu 177 130	17	2 Leu	Ala	Glu	Val	Ser	Arg	Ala	Ala	Asp	Val	His	Ile	Val	Ala	Ala	Thr		
177	17	3		115					120					125					
180 Glu Leu Thr Gln Phe Phe Leu Arg Glu Ile Gln Tyr Gly Ile Glu Asp 160 184 Thr Gly Ile Arg Ala Gly Ile Ile Lys Val Ala Thr Thr Gly Lys Ala 175 175 188 Thr Pro Phe Gln Gln Leu Val Leu Lys Ala Ala Ala Arg Ala Ser Leu Lus Lus	17	Gly	Leu	Trp	Phe	Asp	Pro	Pro	Leu	Ser	Met	Arg	Leu	Arg	Ser	Val	Glu		
181 145	17	7	130					135					140						
184 Thr Gly Ile Arg Ala Gly Ile Lys Val Ala Thr Thr Gly Lys Ala 185 165 165 170 170 175 175 188 Thr Pro Phe Gln Glu Leu Val Leu Lys Ala Ala Arg Ala Ser Leu 189 180 180 Val Thr Thr Thr His Ser Glu Ala Arg Ala Ser Leu 190	18	Glu	Leu	Thr	Gln	Phe	Phe	Leu	Arg	Glu	Ile	Gln	Tyr	Gly	Ile	Glu	Asp		
185																			
188 Thr Pro Phe Gln Glu Leu Val Leu Lys Ala Ala Ala Arg Ala Ser Leu 189 192 Ala Thr Gly Val Pro Val Thr Thr His Thr Ala Ala Ala Ala Asp 190 Asp Asp Asp 190 Asp A	18	1 Thr	Gly	Ile	Arg	Ala	Gly	Ile	Ile	Lys	Val	Ala	Thr	Thr	Gly	Lys	Ala		
189 180 185 190 192 Ala Thr Gly Val Pro Val Thr Thr Thr Thr His Thr Ala Ala Ser Gln Arg Asp 193 195 200 205 196 Gly Glu Gln Gln Ala Ala Ala Ile Phe Glu Ser Glu Gly Leu Ser Pro Ser 197 210 215 220 200 230 220 220 201 225 230 230 235 240 204 Thr Ala Leu Ala Ala Arg Gly Tyr Leu Ile Gly Leu Asp Asp Asp His Ile Pro 250 245 250 250 255 208 His Ser Ala Ile Gly Leu Glu Asp Asp Asn Ala Ser Ala Ser Ala Leu Leu Leu 209 260 265 270 270 212 Gly Ile Arg Ser Trp Gln Thr Arg Ala Leu Leu 11e Lys Ala Leu Ile 23 275 280 280 285 285 216 Asp Gln Gly Tyr Met Lys Gln Ile Leu Val Ser Asp Asp Trp Leu Phe 300 300 295 300 220 Gly Phe Ser Ser Tyr Val Thr Asp Ile Met Asp Val Met Asp Arg Val 320 320																			
192 Ala Thr Gly Val Pro Val Thr Thr His Thr Ala Ala Ser Gln Arg Asp 193	18	3 Thr	Pro	Phe	Gln	Glu	Leu	Val	Leu	Lys	Ala	Ala	Ala	Arg	Ala	Ser	Leu		
193																			
196 Gly Glu Gln Gln Ala Ala Ile Phe Glu Ser Glu Gly Leu Ser Pro Ser 197			Thr	_	Val	Pro	Val	Thr		His	Thr	Ala	Ala		Gln	Arg	Asp		
197												_							
200 Arg Val Cys Ile Gly His Ser Asp Asp Thr Asp Asp Leu Ser Tyr Leu 230		_		Gln	Gln	Ala	Ala		Phe	Glu	Ser	Glu	-	Leu	Ser	Pro	Ser		
201 225																			
204 Thr Ala Leu Ala Ala Arg Gly Tyr Leu Ile Gly Leu Asp His Ile Pro 205		_	Val	Cys	Ile	Gly		Ser	Asp	Asp	Thr		Asp	Leu	Ser	Tyr			
205						_		_			_					_			
208 His Ser Ala Ile Gly Leu Glu Asp Asn Ala Ser Ala Ser Ala Leu Leu 209			Ala	Leu	Ala		Arg	Gly	Tyr	Leu		Gly	Leu	Asp	His		Pro		
209							_					_		_			_		
212 Gly Ile Arg Ser Trp Gln Thr Arg Ala Leu Leu Ile Lys Ala Leu Ile 213 275 280 285 285 216 Asp Gln Gly Tyr Met Lys Gln Ile Leu Val Ser Asn Asp Trp Leu Phe 217 290 295 300 220 Gly Phe Ser Ser Tyr Val Thr Asn Ile Met Asp Val Met Asp Arg Val 221 305 310 310 315 320			Ser	Ala		Gly	Leu	Glu	Asp		Ala	Ser	Ala	Ser		Leu	Leu		
213 275 280 285 216 Asp Gln Gly Tyr Met Lys Gln Ile Leu Val Ser Asn Asp Trp Leu Phe 217 290 295 300 220 Gly Phe Ser Ser Tyr Val Thr Asn Ile Met Asp Val Met Asp Arg Val 221 305 310 320				_		_			_		_	_		_		_			
216 Asp Gln Gly Tyr Met Lys Gln Ile Leu Val Ser Asn Asp Trp Leu Phe 217 290 295 300 220 Gly Phe Ser Ser Tyr Val Thr Asn Ile Met Asp Val Met Asp Arg Val 221 305 310 320		_	Ile	_	Ser	Trp	Gln	Thr	-	Ala	Leu	Leu	Ile		Ala	Leu	TIE		
217 290 295 300 220 Gly Phe Ser Ser Tyr Val Thr Asn Ile Met Asp Val Met Asp Arg Val 221 305 310 315 320					_		_			_		_	_		_	_	_1		
220 Gly Phe Ser Ser Tyr Val Thr Asn Ile Met Asp Val Met Asp Arg Val 221 305 310 315 320		_		Gly	Tyr	Met	Lys		Ile	Leu	Val	Ser		Asp	Trp	Leu	Phe		
221 305 310 315 320				_	_	_			_			_			_	_	7		
		_	Phe	Ser	Ser	Tyr		Thr	Asn	He	Met	_	Val	Met	Asp	Arg			
224 Asn Pro Asp Gly Met Ala Phe Ile Pro Leu Arg Val Ile Pro Phe Leu			_	_	~~			-1		_	_				_	-1			
	22	Asn	Pro	Asp	GIY	Met	Ala	Pne	тте	Pro	ьeu	Arg	val	тте	Pro	Pne	ьeu		

RAW SEQUENCE LISTING

DATE: 11/10/2005

PATENT APPLICATION: US/08/252,384C

TIME: 12:22:35

Input Set : A:\seq listing.txt

225	Olu Ive (325	Pro Gln	Glu Thr	330 Leu Ala Gl	v Ile Th	335
229 Arg (-	340	rio din	345	neu Ara Gr	350	
232 Asn 1 233	Pro Ala A 355	Arg Phe	Leu Ser	Pro Thr 360	Leu Arg Al	a Ser 365	

VERIFICATION SUMMARYDATE: 11/10/2005PATENT APPLICATION: US/08/252,384CTIME: 12:22:36

Input Set : A:\seq listing.txt